

BE #6



PCT10

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/089,014

DATE: 12/02/2002

TIME: 15:26:42

Input Set : A:\11283-019US1.TXT

Output Set: N:\CRF4\12022002\J089014.raw

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4 <110> APPLICANT: Nakayama, Ken-ichi
5      Jigami, Yoshifumi
7 <120> TITLE OF INVENTION: GDP-4-KETO-6-DEOXY-D-MANNOSE-3,
8      5-EPIMERASE-4-REDUCTASE GENE DERIVED FROM ARABIDOPSIS
9      THALIANA
11 <130> FILE REFERENCE: 11283-019US1
13 <140> CURRENT APPLICATION NUMBER: US 10/089,014
14 <141> CURRENT FILING DATE: 2002-03-05
16 <150> PRIOR APPLICATION NUMBER: PCT/JP00/02049
17 <151> PRIOR FILING DATE: 2000-03-30
19 <150> PRIOR APPLICATION NUMBER: JP 329045/1999
20 <151> PRIOR FILING DATE: 1999-11-19
22 <160> NUMBER OF SEQ ID NOS: 6
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 312
28 <212> TYPE: PRT
29 <213> ORGANISM: Arabidopsis thaliana
31 <400> SEQUENCE: 1
32 Met Ser Asp Lys Ser Ala Lys Ile Phe Val Ala Gly His Arg Gly Leu
33 1          5          10          15
34 Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn
35          20          25          30
36 Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp
37          35          40          45
38 Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala
39          50          55          60
40 Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp
41 65          70          75          80
42 Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala
43          85          90          95
44 Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile
45          100         105         110
46 Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr
47          115         120         125
48 Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala
49          130         135         140
50 Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala
51 145         150         155         160
52 Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His
53          165         170         175
54 Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu
55          180         185         190

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56 Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser
57      195      200      205
58 Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val
59      210      215      220
60 Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser
61 225      230      235      240
62 Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val
63      245      250      255
64 Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly
65      260      265      270
66 Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp
67      275      280      285
68 Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp
69      290      295      300
70 Tyr Leu Lys Asn Val Cys Asn Arg
71 305      310
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 936
75 <212> TYPE: DNA
76 <213> ORGANISM: Arabidopsis thaliana
78 <220> FEATURE:
79 <221> NAME/KEY: CDS
80 <222> LOCATION: (1)...(936)
82 <400> SEQUENCE: 2
83 atg tct gac aaa tct gcc aaa atc ttc gtc gcg ggt cat cgt ggt ttg      48
84 Met Ser Asp Lys Ser Ala Lys Ile Phe Val Ala Gly His Arg Gly Leu
85 1      5      10      15
87 gtt gga tct gcc att gtc cgc aag ctt cag gaa caa ggt ttc acc aat      96
88 Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn
89      20      25      30
91 ctc gtt ctt aaa aca cac gcc gag ctt gat ctc act cgt caa gcc gat      144
92 Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp
93      35      40      45
95 gtt gaa tcc ttc ttt tct caa gag aag cca gtt tat gta atc cta gca      192
96 Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala
97      50      55      60
99 gca gct aaa gtt ggt ggt att cac gct aac aac acc tat cct gct gat      240
100 Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp
101 65      70      75      80
103 ttc att ggt gtc aat ctc cag att cag acc aat gtg atc cac tct gca      288
104 Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala
105      85      90      95
107 tat gag cac ggt gtg aag aag ctt ctc ttc ctt gga tca tcc tgc att      336
108 Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile
109      100      105      110
111 tac cct aaa ttt gct cct cag cca att cct gag tct gct ttg tta aca      384
112 Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr
113      115      120      125
115 gca tcg ctt gaa cca act aat gag tgg tat gct att gct aag atc gct      432

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116 Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala
117      130                      135                      140
119 ggg att aag act tgt cag gct tat agg att cag cac gga tgg gat gca      480
120 Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala
121 145                      150                      155                      160
123 atc tct ggc atg cct act aat ctc tat ggt cct aat gac aat ttc cac      528
124 Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His
125                      165                      170                      175
127 ccg gag aat tct cat gtg ctt cct gct ctt atg agg agg ttc cac gag      576
128 Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu
129                      180                      185                      190
131 gcg aaa gtg aat gga gcg gag gaa gtt gtg gtg tgg ggt aca ggt agt      624
132 Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser
133      195                      200                      205
135 ccg ttg agg gag ttc ttg cat gtt gat gat ttg gct gat gct tgt gtt      672
136 Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val
137      210                      215                      220
139 ttc ttg ctg gat cga tac agc ggg ttg gag cat gtt aac att gga agt      720
140 Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser
141 225                      230                      235                      240
143 ggt caa gaa gtg act att aga gag ttg gct gag ttg gtg aaa gag gtt      768
144 Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val
145                      245                      250                      255
147 gtt ggt ttt gaa ggg aag ctt gga tgg gat tgc act aag cca gat ggc      816
148 Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly
149      260                      265                      270
151 aca ccg agg aaa ctt atg gac agc tca aag ctc gcg tct ttg ggt tgg      864
152 Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp
153      275                      280                      285
155 aca cct aag gtt tct ctt aga gat ggt ctg agc caa act tat gat tgg      912
156 Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp
157      290                      295                      300
159 tat ttg aag aat gtt tgc aac cga      936
160 Tyr Leu Lys Asn Val Cys Asn Arg
161 305                      310
164 <210> SEQ ID NO: 3
165 <211> LENGTH: 39
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <223> OTHER INFORMATION: primer
172 <400> SEQUENCE: 3
173 attggtacca tgtctgacaa atctgccaaa atcttcgctc      39
175 <210> SEQ ID NO: 4
176 <211> LENGTH: 50
177 <212> TYPE: DNA
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: primer

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183 <400> SEQUENCE: 4
184 ttagtcgacg atatctcggt tgcaaacatt cttcaaatac caatcataag 50
186 <210> SEQ ID NO: 5
187 <211> LENGTH: 27
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
192 <223> OTHER INFORMATION: primer
194 <400> SEQUENCE: 5
195 gtcgaattca tggcgtcaga gaacaac 27
197 <210> SEQ ID NO: 6
198 <211> LENGTH: 27
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: primer
205 <400> SEQUENCE: 6
206 gaactcgaga ggttgctgct tagcatc 27

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/089,014

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Input Set : A:\11283-019US1.TXT

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